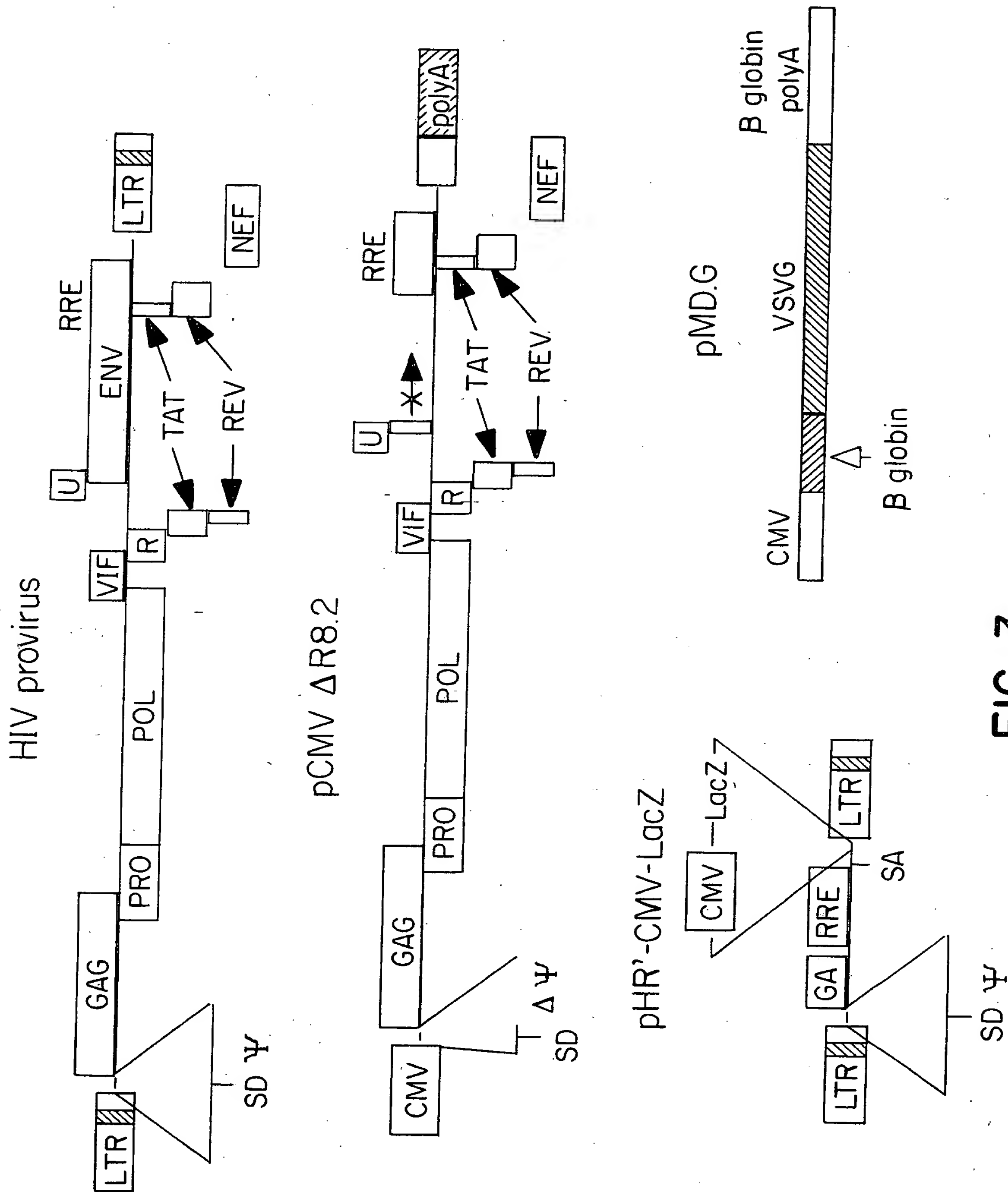


FIG. 1



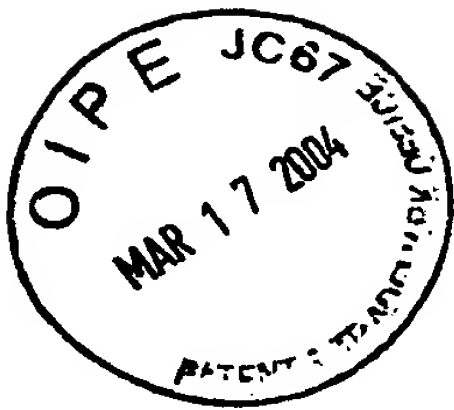


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Alignment Report of Codon optimization (gag).MEG, using Clustal method with PAM250 residue weight table.

810																
792	M	G	A	R	A	S	V	L	S	G	G	E	L	D	K	NL4-3 genbank.SEQ
792	ATG	GGT	GCG	AGA	GCG	TCG	GTA	TTA	AGC	GGG	GGA	GAA	TTA	GAT	AAA	
1319	M	G	A	R	A	S	V	L	S	G	G	E	L	D	K	pHDMHgpm2.seq
1319	ATG	GGC	GCC	CGC	GCC	TCC	GTG	CTG	TCC	GGC	GGC	GAG	CTG	GAC	AAG	
840																
870																
837	W	E	K	I	R	L	R	P	G	G	K	K	Q	Y	K	NL4-3 genbank.SEQ
837	TGG	GAA	AAA	ATT	CGG	TTA	AGG	CCA	GGG	GGA	AAG	AAA	CAA	TAT	AAA	
1364	W	E	K	I	R	L	R	P	G	G	K	K	Q	Y	K	pHDMHgpm2.seq
1364	TGG	GAG	AAG	ATC	CGC	CTG	CGC	CCC	GGC	GGC	AAG	AAG	CAG	TAC	AAG	
900																
882	L	K	H	I	V	W	A	S	R	E	L	E	R	F	A	NL4-3 genbank.SEQ
882	CTA	AAA	CAT	ATA	GTA	TGG	GCA	AGC	AGG	GAG	CTA	GAA	CGA	TTC	GCA	
1409	L	K	H	I	V	W	A	S	R	E	L	E	R	F	A	pHDMHgpm2.seq
1409	CTG	AAG	CAC	ATC	GTG	TGG	GCC	TCC	CGC	GAG	CTG	GAG	CGC	TTC	GCC	
930																
960																
927	V	N	P	G	L	L	E	T	S	E	G	C	R	Q	I	NL4-3 genbank.SEQ
927	GTT	AAT	CCT	GGC	CTT	TTA	GAG	ACA	TCA	GAA	GGC	TGT	AGA	CAA	ATA	
1454	V	N	P	G	L	L	E	T	S	E	G	C	R	Q	I	pHDMHgpm2.seq
1454	GTG	AAC	CCC	GGC	CTG	CTG	GAG	ACC	TCC	GAG	GGC	TGC	CGC	CAG	ATC	
990																
972	L	G	Q	L	Q	P	S	L	Q	T	G	S	E	E	L	NL4-3 genbank.SEQ
972	CTG	GGA	CAG	CTA	CAA	CCA	TCC	CTT	CAG	ACA	GGA	TCA	GAA	GAA	CTT	
1499	L	G	Q	L	Q	P	S	L	Q	T	G	S	E	E	L	pHDMHgpm2.seq
1499	CTG	GGC	CAG	CTG	CAG	CCC	TCC	CTG	CAA	ACC	GGC	TCC	GAG	GAG	CTG	
1020																
1050																
1017	R	S	L	Y	N	T	I	A	V	L	Y	C	V	H	Q	NL4-3 genbank.SEQ
1017	AGA	TCA	TTA	TAT	AAT	ACA	ATA	GCA	GTC	CTC	TAT	TGT	GTG	CAT	CAA	
1544	R	S	L	Y	N	T	I	A	V	L	Y	C	V	H	Q	pHDMHgpm2.seq
1544	CGC	TCC	CTG	TAC	AAC	ACC	ATC	GCC	GTG	CTG	TAC	TGC	GTG	CAC	CAG	
1080																
1062	R	I	D	V	K	D	T	K	E	A	L	D	K	I	E	NL4-3 genbank.SEQ
1062	AGG	ATA	GAT	GTA	AAA	GAC	ACC	AAG	GAA	GCC	TTA	GAT	AAG	ATA	GAG	
1589	R	I	D	V	K	D	T	K	E	A	L	D	K	I	E	pHDMHgpm2.seq
1589	CGC	ATC	GAC	GTG	AAG	GAC	ACC	AAG	GAG	GCC	CTG	GAC	AAG	ATC	GAG	
1110																
1140																
1107	E	E	Q	N	K	S	K	K	K	A	Q	Q	A	A	A	NL4-3 genbank.SEQ
1107	GAA	GAG	CAA	AAC	AAA	AGT	AAG	AAA	AAG	GCA	CAG	CAA	GCA	GCA	GCT	
1634	E	E	Q	N	K	S	K	K	K	A	Q	Q	A	A	A	pHDMHgpm2.seq
1634	GAG	GAG	CAG	AAC	AAG	TCC	AAG	AAG	AAG	GCC	CAG	CAG	GCC	GCC	GCC	

FIG. 8A



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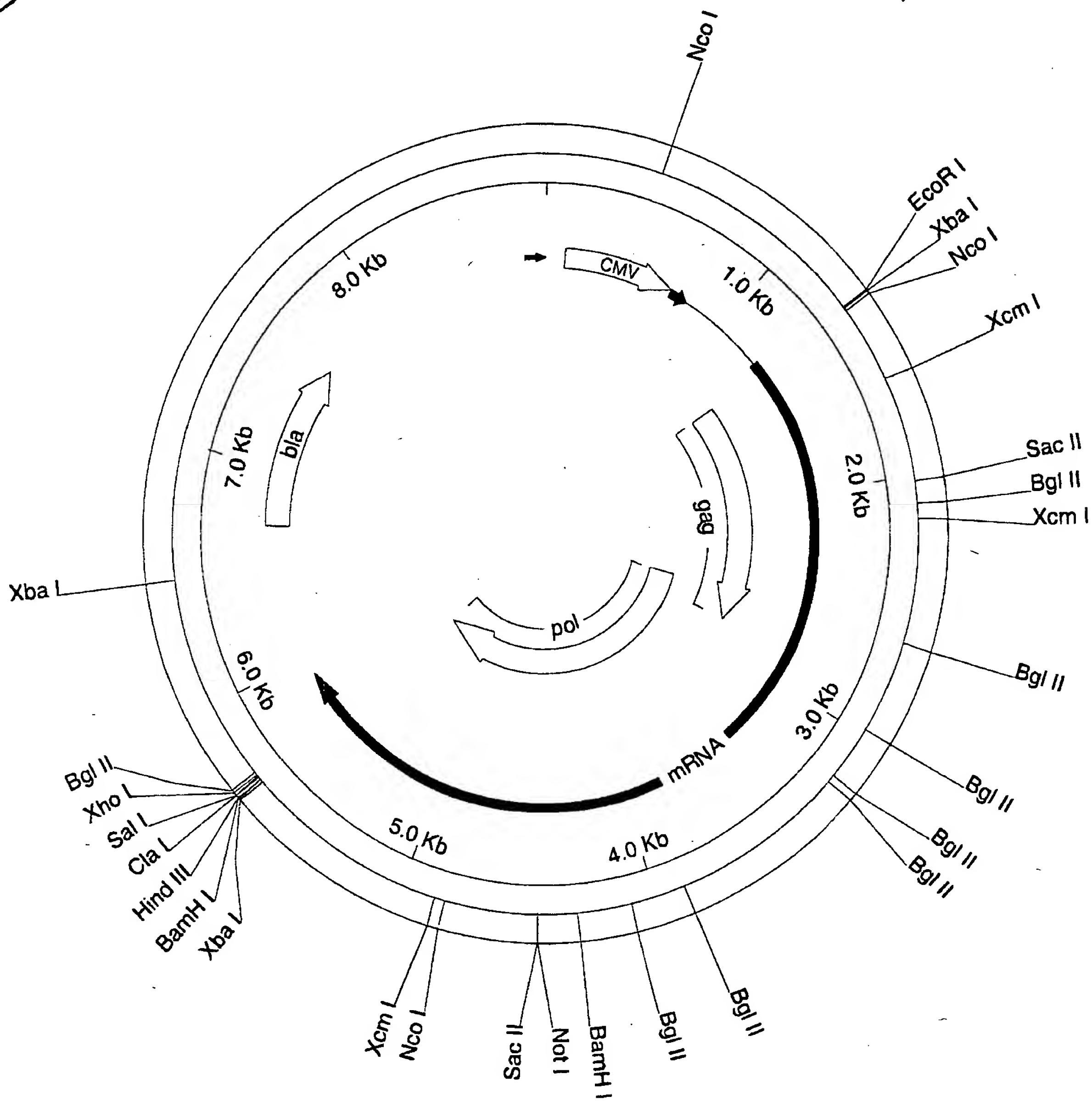


FIG. 11